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Asp Tyr Lys Asp As
p Asp Asp Lys

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0 - 0 0 0 0 0 0 0
0
0 0 0 0 0 0 0 0 0 - 0
0 - 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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$\frac{1}{n} \sum_{i=1}^n x_i - \frac{1}{n} \sum_{i=1}^n y_i$

$\frac{1}{n} \sum_{i=1}^n x_i$

$\frac{1}{n} \sum_{i=1}^n y_i$

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第1表 本発明分子ヒトデルター2の液体培養に対する効果

	全細胞数	コロニー形成細胞	LTC-IC
培養前区	16200	2500	150
培養後			
比較区	445000	23000	2.3
HD1EX1g区	395000	16700	9.3
HD2EX1g区	418000	16000	16.2

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$\frac{1}{n} \sum_{i=1}^n x_i = \bar{x}$

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$\frac{1}{n} \sum_{i=1}^n x_i = \bar{x}$

$\frac{1}{\text{m}^3} \times 10^6 = 10^6 \mu\text{m}^3/\text{m}^3$

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$\frac{1}{n} \sum_{i=1}^n x_i = \bar{x}$

$\alpha - \frac{1}{5} = \frac{1}{5}$

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配列表

配列番号 : 1

配列の長さ : 191

配列の型 : アミノ酸

トポロジー : 直鎖状

配列の種類 : ペプチド

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起源

生物名 : ヒト

配列

Ser Gly Val Phe Gln Leu Gln Leu Gln Glu Phe Ile Asn Glu Arg Gly

1 5 10 15

Val Leu Ala Ser Gly Arg Pro Cys Glu Pro Gly Cys Arg Thr Phe Phe

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20 25 30

Arg Val Cys Leu Lys His Phe Gln Ala Val Val Ser Pro Gly Pro Cys

35 40 45

Thr Phe Gly Thr Val Ser Thr Pro Val Leu Gly Thr Asn Ser Phe Ala

50 55 60

Val Arg Asp Asp Ser Ser Gly Gly Gly Arg Asn Pro Leu Gln Leu Pro

30

65 70 75 80

Phe Asn Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Trp

85 90 95

His Ala Pro Gly Asp Asp Leu Arg Pro Glu Ala Leu Pro Pro Asp Ala

100 105 110

Leu Ile Ser Lys Ile Ala Ile Gln Gly Ser Leu Ala Val Gly Gln Asn

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115 120 125

Trp Leu Leu Asp Glu Gln Thr Ser Thr Leu Thr Arg Leu Arg Tyr Ser

130 135 140

Tyr Arg Val Ile Cys Ser Asp Asn Tyr Tyr Gly Asp Asn Cys Ser Arg

145 150 155 160
 Leu Cys Lys Lys Arg Asn Asp His Phe Gly His Tyr Val Cys Gln Pro
 165 170 175
 Asp Gly Asn Leu Ser Cys Leu Pro Gly Trp Thr Gly Glu Tyr Cys
 180 185 190 191

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配列番号 : 2

配列の長さ : 5 0 0

配列の型 : アミノ酸

トポロジー: 直鎖状

配列の種類 : ペプチド

起源

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生物名 : ヒト

配列

Ser Gly Val Phe Gln Leu Gln Leu Gln Glu Phe Ile Asn Glu Arg Gly
 1 5 10 15
 Val Leu Ala Ser Gly Arg Pro Cys Glu Pro Gly Cys Arg Thr Phe Phe
 20 25 30
 Arg Val Cys Leu Lys His Phe Gln Ala Val Val Ser Pro Gly Pro Cys
 35 40 45
 Thr Phe Gly Thr Val Ser Thr Pro Val Leu Gly Thr Asn Ser Phe Ala
 50 55 60
 Val Arg Asp Asp Ser Ser Gly Gly Gly Arg Asn Pro Leu Gln Leu Pro
 65 70 75 80
 Phe Asn Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Trp
 85 90 95
 His Ala Pro Gly Asp Asp Leu Arg Pro Glu Ala Leu Pro Pro Asp Ala
 100 105 110

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Leu Ile Ser Lys Ile Ala Ile Gln Gly Ser Leu Ala Val Gly Gln Asn
 115 120 125
 Trp Leu Leu Asp Glu Gln Thr Ser Thr Leu Thr Arg Leu Arg Tyr Ser
 130 135 140
 Tyr Arg Val Ile Cys Ser Asp Asn Tyr Tyr Gly Asp Asn Cys Ser Arg
 145 150 155 160
 Leu Cys Lys Lys Arg Asn Asp His Phe Gly His Tyr Val Cys Gln Pro
 165 170 175
 Asp Gly Asn Leu Ser Cys Leu Pro Gly Trp Thr Gly Glu Tyr Cys Gln
 180 185 190
 Gln Pro Ile Cys Leu Ser Gly Cys His Glu Gln Asn Gly Tyr Cys Ser
 195 200 205
 Lys Pro Ala Glu Cys Leu Cys Arg Pro Gly Trp Gln Gly Arg Leu Cys
 210 215 220
 Asn Glu Cys Ile Pro His Asn Gly Cys Arg His Gly Thr Cys Ser Thr
 225 230 235 240
 Pro Trp Gln Cys Thr Cys Asp Glu Gly Trp Gly Gly Leu Phe Cys Asp
 245 250 255
 Gln Asp Leu Asn Tyr Cys Thr His His Ser Pro Cys Lys Asn Gly Ala
 260 265 270
 Thr Cys Ser Asn Ser Gly Gln Arg Ser Tyr Thr Cys Thr Cys Arg Pro
 275 280 285
 Gly Tyr Thr Gly Val Asp Cys Glu Leu Glu Leu Ser Glu Cys Asp Ser
 290 295 300
 Asn Pro Cys Arg Asn Gly Gly Ser Cys Lys Asp Gln Glu Asp Gly Tyr
 305 310 315 320
 His Cys Leu Cys Pro Pro Gly Tyr Tyr Gly Leu His Cys Glu His Ser
 325 330 335

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Thr Leu Ser Cys Ala Asp Ser Pro Cys Phe Asn Gly Gly Ser Cys Arg
340 345 350
Glu Arg Asn Gln Gly Ala Asn Tyr Ala Cys Glu Cys Pro Pro Asn Phe
355 360 365
Thr Gly Ser Asn Cys Glu Lys Lys Val Asp Arg Cys Thr Ser Asn Pro
370 375 380
Cys Ala Asn Gly Gly Gln Cys Leu Asn Arg Gly Pro Ser Arg Met Cys
385 390 395 400
Arg Cys Arg Pro Gly Phe Thr Gly Thr Tyr Cys Glu Leu His Val Ser
405 410 415
Asp Cys Ala Arg Asn Pro Cys Ala His Gly Gly Thr Cys His Asp Leu
420 425 430
Glu Asn Gly Leu Met Cys Thr Cys Pro Ala Gly Phe Ser Gly Arg Arg
435 440 445
Cys Glu Val Arg Thr Ser Ile Asp Ala Cys Ala Ser Ser Pro Cys Phe
450 455 460
Asn Arg Ala Thr Cys Tyr Thr Asp Leu Ser Thr Asp Thr Phe Val Cys
465 470 475 480
Asn Cys Pro Tyr Gly Phe Val Gly Ser Arg Cys Glu Phe Pro Val Gly
485 490 495
Leu Pro Pro Ser
500

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配列番号 : 3

配列の長さ : 6 5 9

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配列の型 : アミノ酸

トポロジー : 直鎖状

配列の種類 : ペプチド

起源

生物名：ヒト

配列

Ser Gly Val Phe Gln Leu Gln Leu Gln Glu Phe Ile Asn Glu Arg Gly	
1 5 10 15	
Val Leu Ala Ser Gly Arg Pro Cys Glu Pro Gly Cys Arg Thr Phe Phe	10
20 25 30	
Arg Val Cys Leu Lys His Phe Gln Ala Val Val Ser Pro Gly Pro Cys	
35 40 45	
Thr Phe Gly Thr Val Ser Thr Pro Val Leu Gly Thr Asn Ser Phe Ala	
50 55 60	
Val Arg Asp Asp Ser Ser Gly Gly Gly Arg Asn Pro Leu Gln Leu Pro	20
65 70 75 80	
Phe Asn Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Trp	
85 90 95	
His Ala Pro Gly Asp Asp Leu Arg Pro Glu Ala Leu Pro Pro Asp Ala	
100 105 110	
Leu Ile Ser Lys Ile Ala Ile Gln Gly Ser Leu Ala Val Gly Gln Asn	30
115 120 125	
Trp Leu Leu Asp Glu Gln Thr Ser Thr Leu Thr Arg Leu Arg Tyr Ser	
130 135 140	
Tyr Arg Val Ile Cys Ser Asp Asn Tyr Tyr Gly Asp Asn Cys Ser Arg	
145 150 155 160	
Leu Cys Lys Lys Arg Asn Asp His Phe Gly His Tyr Val Cys Gln Pro	
165 170 175	40
Asp Gly Asn Leu Ser Cys Leu Pro Gly Trp Thr Gly Glu Tyr Cys Gln	
180 185 190	
Gln Pro Ile Cys Leu Ser Gly Cys His Glu Gln Asn Gly Tyr Cys Ser	

195	200	205	
Lys Pro Ala Glu Cys Leu Cys Arg Pro Gly Trp Gln Gly Arg Leu Cys			
210	215	220	
Asn Glu Cys Ile Pro His Asn Gly Cys Arg His Gly Thr Cys Ser Thr			
225	230	235	240
Pro Trp Gln Cys Thr Cys Asp Glu Gly Trp Gly Gly Leu Phe Cys Asp			10
245	250	255	
Gln Asp Leu Asn Tyr Cys Thr His His Ser Pro Cys Lys Asn Gly Ala			
260	265	270	
Thr Cys Ser Asn Ser Gly Gln Arg Ser Tyr Thr Cys Thr Cys Arg Pro			
275	280	285	
Gly Tyr Thr Gly Val Asp Cys Glu Leu Glu Leu Ser Glu Cys Asp Ser			20
290	295	300	
Asn Pro Cys Arg Asn Gly Gly Ser Cys Lys Asp Gln Glu Asp Gly Tyr			
305	310	315	320
His Cys Leu Cys Pro Pro Gly Tyr Tyr Gly Leu His Cys Glu His Ser			
325	330	335	
Thr Leu Ser Cys Ala Asp Ser Pro Cys Phe Asn Gly Gly Ser Cys Arg			30
340	345	350	
Glu Arg Asn Gln Gly Ala Asn Tyr Ala Cys Glu Cys Pro Pro Asn Phe			
355	360	365	
Thr Gly Ser Asn Cys Glu Lys Lys Val Asp Arg Cys Thr Ser Asn Pro			
370	375	380	
Cys Ala Asn Gly Gly Gln Cys Leu Asn Arg Gly Pro Ser Arg Met Cys			
385	390	395	40
Arg Cys Arg Pro Gly Phe Thr Gly Thr Tyr Cys Glu Leu His Val Ser			
405	410	415	
Asp Cys Ala Arg Asn Pro Cys Ala His Gly Gly Thr Cys His Asp Leu			

420	425	430	
Glu Asn Gly Leu Met Cys Thr Cys Pro Ala Gly Phe Ser Gly Arg Arg			
435	440	445	
Cys Glu Val Arg Thr Ser Ile Asp Ala Cys Ala Ser Ser Pro Cys Phe			
450	455	460	
Asn Arg Ala Thr Cys Tyr Thr Asp Leu Ser Thr Asp Thr Phe Val Cys			10
465	470	475	480
Asn Cys Pro Tyr Gly Phe Val Gly Ser Arg Cys Glu Phe Pro Val Gly			
485	490	495	
Leu Pro Pro Ser Phe Pro Trp Val Ala Val Ser Leu Gly Val Gly Leu			
500	505	510	
Ala Val Leu Leu Val Leu Leu Gly Met Val Ala Val Ala Val Arg Gln			20
515	520	525	
Leu Arg Leu Arg Arg Pro Asp Asp Gly Ser Arg Glu Ala Met Asn Asn			
530	535	540	
Leu Ser Asp Phe Gln Lys Asp Asn Leu Ile Pro Ala Ala Gln Leu Lys			
545	550	555	560
Asn Thr Asn Gln Lys Lys Glu Leu Glu Val Asp Cys Gly Leu Asp Lys			30
565	570	575	
Ser Asn Cys Gly Lys Gln Gln Asn His Thr Leu Asp Tyr Asn Leu Ala			
580	585	590	
Pro Gly Pro Leu Gly Arg Gly Thr Met Pro Gly Lys Phe Pro His Ser			
595	600	605	
Asp Lys Ser Leu Gly Glu Lys Ala Pro Leu Arg Leu His Ser Glu Lys			40
610	615	620	
Pro Glu Cys Arg Ile Ser Ala Ile Cys Ser Pro Arg Asp Ser Met Tyr			
625	630	635	640
Gln Ser Val Cys Leu Ile Ser Glu Glu Arg Asn Glu Cys Val Ile Ala			

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起源

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GTA CTG GCC AGT GGG CGG CCT TGC GAG CCC GGC TGC CGG ACT TTC TTC 450

Val	Leu	Ala	Ser	Gly	Arg	Pro	Cys	Glu	Pro	Gly	Cys	Arg	Thr	Phe	Phe		
		20						25						30			
CGC	GTC	TGC	CTT	AAG	CAC	TTC	CAG	GCG	GTC	GTC	TCG	CCC	GGA	CCC	TGC	498	
Arg	Val	Cys	Leu	Lys	His	Phe	Gln	Ala	Val	Val	Ser	Pro	Gly	Pro	Cys		
		35						40						45			
ACC	TTC	GGG	ACC	GTC	TCC	ACG	CCG	GTA	TTG	GGC	ACC	AAC	TCC	TTC	GCT	546	10
Thr	Phe	Gly	Thr	Val	Ser	Thr	Pro	Val	Leu	Gly	Thr	Asn	Ser	Phe	Ala		
		50						55						60			
GTC	CGG	GAC	GAC	AGT	AGC	GGC	GGG	GGG	CGC	AAC	CCT	CTC	CAA	CTG	CCC	594	
Val	Arg	Asp	Asp	Ser	Ser	Gly	Gly	Gly	Arg	Asn	Pro	Leu	Gln	Leu	Pro		
		65						70						75			
TTC	AAT	TTC	ACC	TGG	CCG	GGT	ACC	TTC	TCG	CTC	ATC	ATC	GAA	GCT	TGG	642	20
Phe	Asn	Phe	Thr	Trp	Pro	Gly	Thr	Phe	Ser	Leu	Ile	Ile	Glu	Ala	Trp		
				85						90				95			
CAC	GCG	CCA	GGA	GAC	GAC	CTG	CGG	CCA	GAG	GCC	TTG	CCA	CCA	GAT	GCA	690	
His	Ala	Pro	Gly	Asp	Asp	Leu	Arg	Pro	Glu	Ala	Leu	Pro	Pro	Asp	Ala		
		100								105				110			
CTC	ATC	AGC	AAG	ATC	GCC	ATC	CAG	GGC	TCC	CTA	GCT	GTG	GGT	CAG	AAC	738	30
Leu	Ile	Ser	Lys	Ile	Ala	Ile	Gln	Gly	Ser	Leu	Ala	Val	Gly	Gln	Asn		
		115								120				125			
TGG	TTA	TTG	GAT	GAG	CAA	ACC	AGC	ACC	CTC	ACA	AGG	CTG	CGC	TAC	TCT	786	
Trp	Leu	Leu	Asp	Glu	Gln	Thr	Ser	Thr	Leu	Thr	Arg	Leu	Arg	Tyr	Ser		
		130								135				140			
TAC	CGG	GTC	ATC	TGC	AGT	GAC	AAC	TAC	TAT	GGA	GAC	AAC	TGC	TCC	CGC	834	40
Tyr	Arg	Val	Ile	Cys	Ser	Asp	Asn	Tyr	Tyr	Gly	Asp	Asn	Cys	Ser	Arg		
		145								150				155			
CTG	TGC	AAG	AAG	CGC	AAT	GAC	CAC	TTC	GGC	CAC	TAT	GTG	TGC	CAG	CCA	882	
Leu	Cys	Lys	Lys	Arg	Asn	Asp	His	Phe	Gly	His	Tyr	Val	Cys	Gln	Pro		

165	170	175	
GAT GGC AAC TTG TCC TGC CTG CCC GGT TGG ACT GGG GAA TAT TGC CAA	930		
Asp Gly Asn Leu Ser Cys Leu Pro Gly Trp Thr Gly Glu Tyr Cys Gln			
180	185	190	
CAG CCT ATC TGT CTT TCG GGC TGT CAT GAA CAG AAT GGC TAC TGC AGC	978		
Gln Pro Ile Cys Leu Ser Gly Cys His Glu Gln Asn Gly Tyr Cys Ser			10
195	200	205	
AAG CCA GCA GAG TGC CTC TGC CGC CCA GGC TGG CAG GGC CGG CTG TGT	1026		
Lys Pro Ala Glu Cys Leu Cys Arg Pro Gly Trp Gln Gly Arg Leu Cys			
210	215	220	
AAC GAA TGC ATC CCC CAC AAT GGC TGT CGC CAC GGC ACC TGC AGC ACT	1074		
Asn Glu Cys Ile Pro His Asn Gly Cys Arg His Gly Thr Cys Ser Thr			20
225	230	235	240
CCC TGG CAA TGT ACT TGT GAT GAG GGC TGG GGA GGC CTG TTT TGT GAC	1122		
Pro Trp Gln Cys Thr Cys Asp Glu Gly Trp Gly Gly Leu Phe Cys Asp			
245	250	255	
CAA GAT CTC AAC TAC TGC ACC CAC CAC TCC CCA TGC AAG AAT GGG GCA	1170		
Gln Asp Leu Asn Tyr Cys Thr His His Ser Pro Cys Lys Asn Gly Ala			30
260	265	270	
ACG TGC TCC AAC AGT GGG CAG CGA AGC TAC ACC TGC ACC TGT CGC CCA	1218		
Thr Cys Ser Asn Ser Gly Gln Arg Ser Tyr Thr Cys Thr Cys Arg Pro			
275	280	285	
GGC TAC ACT GGT GTG GAC TGT GAG CTG GAG CTC AGC GAG TGT GAC AGC	1266		
Gly Tyr Thr Gly Val Asp Cys Glu Leu Glu Leu Ser Glu Cys Asp Ser			40
290	295	300	
AAC CCC TGT CGC AAT GGA GGC AGC TGT AAG GAC CAG GAG GAT GGC TAC	1314		
Asn Pro Cys Arg Asn Gly Gly Ser Cys Lys Asp Gln Glu Asp Gly Tyr			
305	310	315	320

CAC TGC CTG TGT CCT CCG GGC TAC TAT GGC CTG CAT TGT GAA CAC AGC 1362
His Cys Leu Cys Pro Pro Gly Tyr Tyr Gly Leu His Cys Glu His Ser
325 330 335
ACC TTG AGC TGC GCC GAC TCC CCC TGC TTC AAT GCG GGC TCC TGC CGG 1410
Thr Leu Ser Cys Ala Asp Ser Pro Cys Phe Asn Gly Gly Ser Cys Arg
340 345 350
GAG CGC AAC CAG GGG GCC AAC TAT GCT TGT GAA TGT CCC CCC AAC TTC 1458
Glu Arg Asn Gln Gly Ala Asn Tyr Ala Cys Glu Cys Pro Pro Asn Phe
355 360 365
ACC GGC TCC AAC TGC GAG AAG AAA GTG GAC AGG TGC ACC AGC AAC CCC 1506
Thr Gly Ser Asn Cys Glu Lys Lys Val Asp Arg Cys Thr Ser Asn Pro
370 375 380
TGT GCC AAC GGG GGA CAG TGC CTG AAC CGA GGT CCA AGC CGC ATG TGC 1554
Cys Ala Asn Gly Gly Gln Cys Leu Asn Arg Gly Pro Ser Arg Met Cys
385 390 395 400
CGC TGC CGT CCT GGA TTC ACG GGC ACC TAC TGT GAA CTC CAC GTC AGC 1602
Arg Cys Arg Pro Gly Phe Thr Gly Thr Tyr Cys Glu Leu His Val Ser
405 410 415
GAC TGT GCC CGT AAC CCT TGC GCC CAC GGT GGC ACT TGC CAT GAC CTG 1650
Asp Cys Ala Arg Asn Pro Cys Ala His Gly Gly Thr Cys His Asp Leu
420 425 430
GAG AAT GGG CTC ATG TGC ACC TGC CCT GCC GGC TTC TCT GGC CGA CGC 1698
Glu Asn Gly Leu Met Cys Thr Cys Pro Ala Gly Phe Ser Gly Arg Arg
435 440 445
TGT GAG GTG CGG ACA TCC ATC GAT GCC TGT GCC TCG AGT CCC TGC TTC 1746
Cys Glu Val Arg Thr Ser Ile Asp Ala Cys Ala Ser Ser Pro Cys Phe
450 455 460
AAC AGG GCC ACC TGC TAC ACC GAC CTC TCC ACA GAC ACC TTT GTG TGC 1794

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Asn Arg Ala Thr Cys Tyr Thr Asp Leu Ser Thr Asp Thr Phe Val Cys			
465	470	475	480
AAC TGC CCT TAT GGC TTT GTG GGC AGC CGC TGC GAG TTC CCC GTG GGC	1842		
Asn Cys Pro Tyr Gly Phe Val Gly Ser Arg Cys Glu Phe Pro Val Gly			
485	490	495	
TTG CCG CCC AGC TTC CCC TGG GTG GCC GTC TCG CTG GGT GTG GGG CTG	1890		10
Leu Pro Pro Ser Phe Pro Trp Val Ala Val Ser Leu Gly Val Gly Leu			
500	505	510	
GCA GTG CTG CTG GTA CTG CTG GGC ATG GTG GCA GTG GCT GTG CGG CAG	1938		
Ala Val Leu Leu Val Leu Leu Gly Met Val Ala Val Ala Val Arg Gln			
515	520	525	
CTG CCG CTT CGA CGG CCG GAC GAC GGC AGC AGG GAA GCC ATG AAC AAC	1986		20
Leu Arg Leu Arg Arg Pro Asp Asp Gly Ser Arg Glu Ala Met Asn Asn			
530	535	540	
TTG TCG GAC TTC CAG AAG GAC AAC CTG ATT CCT GCC GCC CAG CTT AAA	2034		
Leu Ser Asp Phe Gln Lys Asp Asn Leu Ile Pro Ala Ala Gln Leu Lys			
545	550	555	560
AAC ACA AAC CAG AAG AAG GAG CTG GAA GTG GAC TGT GGC CTG GAC AAG	2082		
Asn Thr Asn Gln Lys Lys Glu Leu Glu Val Asp Cys Gly Leu Asp Lys			30
565	570	575	
TCC AAC TGT GGC AAA CAG CAA AAC CAC ACA TTG GAC TAT AAT CTG GCC	2130		
Ser Asn Cys Gly Lys Gln Gln Asn His Thr Leu Asp Tyr Asn Leu Ala			
580	585	590	
CCA GGG CCC CTG GGG CGG GGG ACC ATG CCA GGA AAG TTT CCC CAC AGT	2178		
Pro Gly Pro Leu Gly Arg Gly Thr Met Pro Gly Lys Phe Pro His Ser			40
595	600	605	
GAC AAG AGC TTA GGA GAG AAG GCG CCA CTG CGG TTA CAC AGT GAA AAG	2226		
Asp Lys Ser Leu Gly Glu Lys Ala Pro Leu Arg Leu His Ser Glu Lys			

610	615	620	
CCA GAG TGT CGG ATA TCA GCG ATA TGC TCC CCC AGG GAC TCC ATG TAC	2274		
Pro Glu Cys Arg Ile Ser Ala Ile Cys Ser Pro Arg Asp Ser Met Tyr			
625	630	635	640
CAG TCT GTG TGT TTG ATA TCA GAG GAG AGG AAT GAA TGT GTC ATT GCC	2322		
Gln Ser Val Cys Leu Ile Ser Glu Glu Arg Asn Glu Cys Val Ile Ala			10
	645	650	655
ACG GAG GTA			2331
Thr Glu Val			
659			
TAAGGCAGGA GCCTACCTGG ACATCCCTGC TCAGCCCCGC GGCTGGACCT TCCTTCTGCA	2391		
TTGTTTACAT TGCATCCTGG ATGGGACCTT TTTCATATGC AACGTGCTGC TCTCAGGAGG	2451		20
AGGAGGGAAT GGCAGGAACC GGACAGACTG TGAACCTGCC AAGAGATGCA ATACCCTTCC	2511		
ACACCTTTGG GTGTCTGTCT GGCATCAGAT TGGCAGCTGC ACCAACCAGA GGAACAGAAG	2571		
AGAAGAGAGA TGCCACTGGG CACTGCCCTG CCAGTAGTGG CCTTCAGGGG GCTCCTTCCG	2631		
GGGCTCCGGC CTGTTTTCCA GAGAGAGTGG CAGTAGCCCC ATGGGGCCCG GAGCTGCTGT	2691		
GGCCTCCACT GGCATCCGTG TTTCCAAAAG TGCCTTTGGC CCAGGCTCCA CGGCGACAGT	2751		
TGGGCCCCAA TCAGAAAGGA GAGAGGGGGC CAATGAGGGC AGGGCCTCCT GTGGGCTGGA	2811		30
AAACCACTGG GTGCGTCTCT TGCTGGGGTT TGCCCTGGAG GTGAGGTGAG TGCTCGAGGG	2871		
AGGGGAGTGC TTTCTGCCCC ATGCCTCCAA CTACTGTATG CAGGCCTGGC TCTCTGGTCT	2931		
AGGCCCTTTG GGCAAGAATG TCCGTCTACC CGGCTTCCAC CACCCTCTGG CCCTGGGCTT	2991		
CTGTAAGCAG ACAGGCAGAG GGCCTGCCCC TCCCACCAGC CAAGGGTGCC AGGCCTAACT	3051		
GGGGCACTCA GGGCAGTGTG TTGGAAATTC CACTGAGGGG GAAATCAGGT GCTGCGGCCG	3111		
CCTGGGGCCT TTCCTCCCTC AAGCCCATCT CCACAACCTC GAGCCTGGGC TCTGGTCCAC	3171		
TACTGCCCCA GACCACCCTC AAAGCTGGTC TTCAGAAATC AATAATATGA GTTTTTATTT	3231		40
TGTTTTTTTT TTTTTTTTGT TAGTTTATTT TGGAGTCTAG TATTTCAATA ATTTAAGAAT	3291		
CAGAAGCACT GACCTTTCTA CATTTTATAA CATTATTTTG TATATAAT	3339		

配列番号 : 5

配列の長さ : 27

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

10

配列

GAT TAT AAA GAT GAT GAT GAT AAA TGA

27

Asp Tyr Lys Asp Asp Asp Asp Lys

1 5 8

配列番号 : 6

20

配列の長さ : 20

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

配列

TGGCARTGYA AYTGYCARGA

20

30

配列番号 : 7

配列の長さ : 20

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー : 直鎖状

40

配列の種類 : 他の核酸 (化学合成DNA)

配列

ATYTTYTTYT CRCARTTAA

20

配列番号 : 8

配列の長さ : 2 6 6 3

配列の型 : 核酸

鎖の数 : 二本鎖

トポロジー : 直鎖状

配列の種類 : cDNA to mRNA

10

起源

生物名 : ヒト

配列

CTTGGGAA GAGGCGGAGA CCGGCTTTTA AAGAAAGAAG TCCTGGGTCC TGCGGTCTGG	58	
GGCGAGGCAA GGGCGCTTTT CTGCCCACGC TCCCCGTGGC CCATCGATCC CCCGCGCGTC	118	
CGCCGCTGTT CTAAGGAGAG AAGTGGGGGC CCCCCAGGCT CGCGCGTGGA GCGAAGCAGC	178	
ATG GGC AGT CGG TGC GCG CTG GCC CTG GCG GTG CTC TCG GCC TTG CTG	226	20
Met Gly Ser Arg Cys Ala Leu Ala Leu Ala Val Leu Ser Ala Leu Leu		
-20 -15 -10		
TGT CAG GTC TGG AGC TCT GGG GTG TTC GAA CTG AAG CTG CAG GAG TTC	274	
Cys Gln Val Trp Ser Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe		
-5 -1 1 5 10		
GTC AAC AAG AAG GGG CTG CTG GGG AAC CGC AAC TGC TGC CGC GGG GGC	322	30
Val Asn Lys Lys Gly Leu Leu Gly Asn Arg Asn Cys Cys Arg Gly Gly		
15 20 25		
GCG GGG CCA CCG CCG TGC GCC TGC CGG ACC TTC TTC CGC GTG TGC CTC	370	
Ala Gly Pro Pro Pro Cys Ala Cys Arg Thr Phe Phe Arg Val Cys Leu		
30 35 40		
AAG CAC TAC CAG GCC AGC GTG TCC CCC GAG CCG CCC TGC ACC TAC GGC	418	40
Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly		
45 50 55		
AGC GCC GTC ACC CCC GTG CTG GGC GTC GAC TCC TTC AGT CTG CCC GAC	466	

Ser Ala Val Thr Pro Val Leu Gly Val Asp Ser Phe Ser Leu Pro Asp			
60	65	70	75
GGC GGC GGC GCC GAC TCC GCG TTC AGC AAC CCC ATC CGC TTC CCC TTC	514		
Gly Gly Gly Ala Asp Ser Ala Phe Ser Asn Pro Ile Arg Phe Pro Phe			
80	85	90	
GGC TTC ACC TGG CCG GGC ACC TTC TCT CTG ATT ATT GAA GCT CTC CAC	562	10	
Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu His			
95	100	105	
ACA GAT TCT CCT GAT GAC CTC GCA ACA GAA AAC CCA GAA AGA CTC ATC	610		
Thr Asp Ser Pro Asp Asp Leu Ala Thr Glu Asn Pro Glu Arg Leu Ile			
110	115	120	
AGC CGC CTG GCC ACC CAG AGG CAC CTG ACG GTG GGC GAG GAG TGG TCC	658	20	
Ser Arg Leu Ala Thr Gln Arg His Leu Thr Val Gly Glu Glu Trp Ser			
125	130	135	
CAG GAC CTG CAC AGC AGC GGC CGC ACG GAC CTC AAG TAC TCC TAC CGC	706		
Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr Arg			
140	145	150	155
TTC GTG TGT GAC GAA CAC TAC TAC GGA GAG GGC TGC TCC GTT TTC TGC	754	30	
Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe Cys			
160	165	170	
CGT CCC CGG GAC GAT GCC TTC GGC CAC TTC ACC TGT GGG GAG CGT GGG	802		
Arg Pro Arg Asp Asp Ala Phe Gly His Phe Thr Cys Gly Glu Arg Gly			
175	180	185	
GAG AAA GTG TGC AAC CCT GGC TGG AAA GGG CCC TAC TGC ACA GAG CCG	850	40	
Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Pro Tyr Cys Thr Glu Pro			
190	195	200	
ATC TGC CTG CCT GGA TGT GAT GAG CAG CAT GGA TTT TGT GAC AAA CCA	898		
Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys Pro			

205	210	215		
GGG GAA TGC AAG TGC AGA GTG GGC TGG CAG GGC CGG TAC TGT GAC GAG			946	
Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp Glu				
220	225	230	235	
TGT ATC CGC TAT CCA GGC TGT CTC CAT GGC ACC TGC CAG CAG CCC TGG			994	
Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro Trp				10
240	245	250		
CAG TGC AAC TGC CAG GAA GGC TGG GGC GGC CTT TTC TGC AAC CAG GAC			1042	
Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln Asp				
255	260	265		
CTG AAC TAC TGC ACA CAC CAT AAG CCC TGC AAG AAT GGA GCC ACC TGC			1090	
Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr Cys				20
270	275	280		
ACC AAC ACG GGC CAG GGC AGC TAC ACT TGC TCT TGC CGG CCT GGC TAC			1138	
Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly Tyr				
285	290	295		
ACA GGT GCC ACC TGC GAG CTG GGC ATT GAC GAG TGT GAC CCC AGC CCT			1186	
Thr Gly Ala Thr Cys Glu Leu Gly Ile Asp Glu Cys Asp Pro Ser Pro				
300	305	310	315	30
TGT AAG AAC GGA GGC AGC TGC ACG GAT CTC GAG AAC AGC TAC TCC TGT			1234	
Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser Cys				
320	325	330		
ACC TGC CCA CCC GGC TTC TAC GGC AAA ATC TGT GAA TTG AGT GCC ATG			1282	
Thr Cys Pro Pro Gly Phe Tyr Gly Lys Ile Cys Glu Leu Ser Ala Met				
335	340	345		40
ACC TGT GCG GAC GGC CCT TGC TTT AAC GGC GGT CGG TGC TCA GAC AGC			1330	
Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Ser Asp Ser				
350	355	360		

CCC GAT GGA GGG TAC AGC TGC CGC TGC CCC GTG GGC TAC TCC GGC TTC	1378	
Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Val Gly Tyr Ser Gly Phe		
365 370 375		
AAC TGT GAG AAG AAA ATT GAC TAC TGC AGC TCT TCA CCC TGT TCT AAT	1426	
Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ser Asn		
380 385 390 395		10
GGT GCC AAG TGT GTG GAC CTC GGT GAT GCC TAC CTG TGC CGC TGC CAG	1474	
Gly Ala Lys Cys Val Asp Leu Gly Asp Ala Tyr Leu Cys Arg Cys Gln		
400 405 410		
GCC GGC TTC TCG GGG AGG CAC TGT GAC GAC AAC GTG GAC GAC TGC GCC	1522	
Ala Gly Phe Ser Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys Ala		
415 420 425		20
TCC TCC CCG TGC GCC AAC GGG GGC ACC TGC CGG GAT GGC GTG AAC GAC	1570	
Ser Ser Pro Cys Ala Asn Gly Gly Thr Cys Arg Asp Gly Val Asn Asp		
430 435 440		
TTC TCC TGC ACC TGC CCG CCT GGC TAC ACG GGC AGG AAC TGC AGT GCC	1618	
Phe Ser Cys Thr Cys Pro Pro Gly Tyr Thr Gly Arg Asn Cys Ser Ala		
445 450 455		
CCC GTC AGC AGG TGC GAG CAC GCA CCC TGC CAC AAT GGG GCC ACC TGC	1666	30
Pro Val Ser Arg Cys Glu His Ala Pro Cys His Asn Gly Ala Thr Cys		
460 465 470 475		
CAC GAG AGG GGC CAC CGC TAT GTG TGC GAG TGT GCC CGA GGC TAC GGG	1714	
His Glu Arg Gly His Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr Gly		
480 485 490		
GGT CCC AAC TGC CAG TTC CTG CTC CCC GAG CTG CCC CCG GGC CCA GCG	1762	40
Gly Pro Asn Cys Gln Phe Leu Leu Pro Glu Leu Pro Pro Gly Pro Ala		
495 500 505		
GTG GTG GAC CTC ACT GAG AAG CTA GAG GGC CAG GGC GGG CCA TTC CCC	1810	

Val Val Asp Leu Thr Glu Lys Leu Glu Gly Gln Gly Gly Pro Phe Pro			
510	515	520	
TGG GTG GCC GTG TGC GCC GGG GTC ATC CTT GTC CTC ATG CTG CTG CTG	1858		
Trp Val Ala Val Cys Ala Gly Val Ile Leu Val Leu Met Leu Leu Leu			
525	530	535	
GGC TGT GCC GCT GTG GTG GTC TGC GTC CGG CTG AGG CTG CAG AAG CAC	1906	10	
Gly Cys Ala Ala Val Val Val Cys Val Arg Leu Arg Leu Gln Lys His			
540	545	550	555
CGG CCC CCA GCC GAC CCC TGC CGG GGG GAG ACG GAG ACC ATG AAC AAC	1954		
Arg Pro Pro Ala Asp Pro Cys Arg Gly Glu Thr Glu Thr Met Asn Asn			
560	565	570	
CTG GCC AAC TGC CAG CGT GAG AAG GAC ATC TCA GTC AGC ATC ATC GGG	2002	20	
Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Val Ser Ile Ile Gly			
575	580	585	
GCC ACG CAG ATC AAG AAC ACC AAC AAG AAG GCG GAC TTC CAC GGG GAC	2050		
Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Ala Asp Phe His Gly Asp			
590	595	600	
CAC AGC GCC GAC AAG AAT GGC TTC AAG GCC CGC TAC CCA GCG GTG GAC	2098	30	
His Ser Ala Asp Lys Asn Gly Phe Lys Ala Arg Tyr Pro Ala Val Asp			
605	610	615	
TAT AAC CTC GTG CAG GAC CTC AAG GGT GAC GAC ACC GCC GTC AGG GAC	2146		
Tyr Asn Leu Val Gln Asp Leu Lys Gly Asp Asp Thr Ala Val Arg Asp			
620	625	630	635
GCG CAC AGC AAG CGT GAC ACC AAG TGC CAG CCC CAG GGC TCC TCA GGG	2194	40	
Ala His Ser Lys Arg Asp Thr Lys Cys Gln Pro Gln Gly Ser Ser Gly			
640	645	650	
GAG GAG AAG GGG ACC CCG ACC ACA CTC AGG GGT GGA GAA GCA TCT GAA	2242		
Glu Glu Lys Gly Thr Pro Thr Thr Leu Arg Gly Gly Glu Ala Ser Glu			

655	660	665	
AGA AAA AGG CCG GAC TCG GGC TGT TCA ACT TCA AAA GAC ACC AAG TAC	2290		
Arg Lys Arg Pro Asp Ser Gly Cys Ser Thr Ser Lys Asp Thr Lys Tyr			
670	675	680	
CAG TCG GTG TAC GTC ATA TCC GAG GAG AAG GAT GAG TGC GTC ATA GCA	2338		
Gln Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Val Ile Ala			
685	690	695	
ACT GAG GTG			2347
Thr Glu Val			
700			
TAAATGGAA GTGAGATGGC AAGACTCCCG TTTCTCTTAA AATAAGTAAA ATTCCAAGGA	2407		
TATATGCCCC AACGAATGCT GCTGAAGAGG AGGGAGGCCT CGTGGACTGC TGCTGAGAAA	2467		
CCGAGTTCAG ACCGAGCAGG TTCTCCTCCT GAGGTCTCG ACGCCTGCCG ACAGCCTGTC	2527		
GCGGCCCGGC CGCCTGCGGC ACTGCCTTCC GTGACGTCGC CGTTGCACTA TGGACAGTTG	2587		
CTCTTAAGAG AATATATATT TAAATGGGTG AACTGAATTA CGCATAAGAA GCATGCACTG	2647		
CCTGAGTGTA TATTTT	2663		

10

20

配列番号 : 9

配列の長さ : 20

30

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

配列

TGACGGTGGG CGAGGAGTGG

20

40

配列番号 : 10

配列の長さ : 20

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

配列

GCAGCTGTAC CCTCCATCGG

20

10

配列番号 : 1 1

配列の長さ : 7 1 6

配列の型 : 核酸

鎖の数 : 二本鎖

トポロジー : 直鎖状

配列の種類 : cDNA to mRNA

起源 : ヒト

配列

TGACGGTGGG CGAGGAGTGG TCCCAGGACC TGCACAGCAG CGGCCGCACG GACCTCAAGT 60
 ACTCCTACCG CTTCGTGTGT GACGAACACT ACTACGGAGA GGGCTGCTCC GTTTTCTGCC 120
 GTCCCCGGGA CGATGCCTTC GGCCACTTCA CCTGTGGGGA GCGTGGGGAG AAAGTGTGCA 180
 ACCCTGGCTG GAAAGGGCCC TACTGCACAG AGCCGATCTG CCTGCCTGCA TGTGATGAGC 240
 AGCATGGATT TTGTGACAAA CCAGGGGAAT GCAAGTGCAG AGTGGGCTGG CAGGGCCGGT 300
 ACTGTGACGA GTGTATCCGC TATCCAGGCT GTCTCCATGG CACCTGCCAG CAGCCCTGGC 360
 AGTGCAACTG CCAGGAAGGC TGGGGGGGCC TTTTCTGCAA CCAGGACCTG AACTACTGCA 420
 CACACCATAA GCCCTGCAAG AATGGAGCCA CCTGCACCAA CACGGGCCAG GGGAGCTACA 480
 CTTGCTCTTG CCGGCCTGGG TACACAGGTG CCACCTGCCA GCTGGGGATT GACGAGTGTG 540
 ACCCCAGCCC TTGTAAGAAC GGAGGGAGCT GCACGGATCT CGAGAACAGC TACTCCTGTA 600
 CCTGCCCACC CGGCTTCTAC GGCAAAATCT GTGAATTGAG TGCCATGACC TGTGCGGACG 660
 GCCCTTGCTT TAACGGGGGT CGGTGCTCAG ACAGCCCCGA TGGAGGGTAC AGCTGC 716

30

40

配列番号 : 1 2

配列の長さ : 2 0

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

10

配列

TTGGGCACCA ACTCCTTCGC

20

配列番号 : 1 3

配列の長さ : 2 0

配列の型 : 核酸

20

鎖の数 : 一本鎖

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

配列

TAGGCTGTTG GCAATATTCC

20

配列番号 : 1 4

30

配列の長さ : 4 1 2

配列の型 : 核酸

鎖の数 : 二本鎖

トポロジー : 直鎖状

配列の種類 : cDNA to mRNA

起源 : ヒト

40

配列

TTGGGCACCA ACTCCTTCGC TGTCGGGAC GACAGTAGCG GCGGGGGGCG CAACCCTCTC 60

CAACTGCCCT TCAATTTAC CTGGCCGGGT ACCTTCTCGC TCATCATCGA AGCTTGGCAC 120

GCGCCAGGAG ACGACCTGCG GCCAGAGGCC TTGCCACCAG ATGCACTCAT CAGCAAGATC 180
 GCCATCCAGG GCTCCCTAGC TGTGGGTCAG AACTGGTTAT TGGATGAGCA AACCAGCACC 240
 CTCACAAGGC TGCCTACTC TTACCGGGTC ATCTGCAGTG ACAACTACTA TGGAGACAAC 300
 TGCTCCCGCC TGTGCAAGAA GCGCAATGAC CACTTCGGCC ACTATGTGTG CCAGCCAGAT 360
 GGCAACTTGT CCTGCCTGCC CGGTTGGACT GGGGAATATT GCCAACAGCC TA 412

10

配列番号 : 1 5

配列の長さ : 2 8

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

20

配列

CGGCGACGCC CGAGGGGATG GCGGCAGC 28

配列番号 : 1 6

配列の長さ : 3 0

配列の型 : 核酸

鎖の数 : 一本鎖

30

トポロジー : 直鎖状

配列の種類 : 他の核酸 (化学合成DNA)

配列

GAATTCCACC GCGGTGGAGC TCCAATTCGC 30

配列番号 : 1 7

40

配列の長さ : 2 8

配列の型 : 核酸

鎖の数 : 一本鎖

トポロジー：直鎖状

配列の種類：他の核酸（化学合成DNA）

配列

TCAGCTGGGC GGCAAGCCCA CGGGGAAC

28

配列番号：18

10

配列の長さ：33

配列の型：核酸

鎖の数：一本鎖

トポロジー：直鎖状

配列の種類：他の核酸（化学合成DNA）

配列

GCGGCCGCTT ATCGATACCG TCGACCTCGA GGG

33

20

配列番号19

配列の長さ：52

配列の型：核酸

鎖の数：一本鎖

トポロジー：直鎖状

30

配列の種類：他の核酸（化学合成DNA）

配列

TCATTTATCA TCATCATCTT TATAATCGCT GGGCGGCAAG CCCACGGGGA AC

52

配列番号：20

配列の長さ：36

40

配列の型：核酸

鎖の数：一本鎖

トポロジー：直鎖状

配列の種類：他の核酸（化学合成DNA）

配列

AAAGGATCCG AGGGCGGCAA GCCCACGGGG AACTCG 36

配列番号：21

配列の長さ：25

10

配列の型：核酸

鎖の数：一本鎖

トポロジー：直鎖状

配列の種類：他の核酸（化学合成DNA）

配列

TTATACCTCC GTGGCAATGA CACAT 25

20

配列番号：22

配列の長さ：52

配列の型：核酸

鎖の数：一本鎖

トポロジー：直鎖状

配列の種類：他の核酸（化学合成DNA）

30

配列

TCATTTATCA TCATCATCTT TATAATCTAC CTCGGTGGCA ATGACACATT CA 52

配列番号：23

配列の長さ：36

配列の型：核酸

40

鎖の数：一本鎖

トポロジー：直鎖状

配列の種類：他の核酸（化学合成DNA）

36

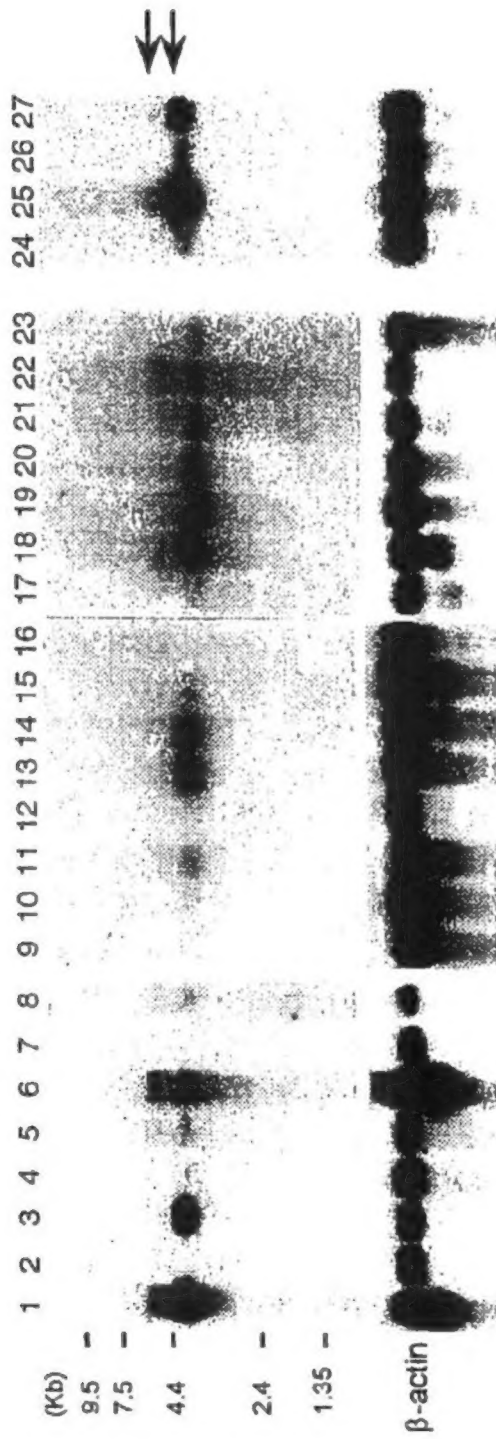
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33

20

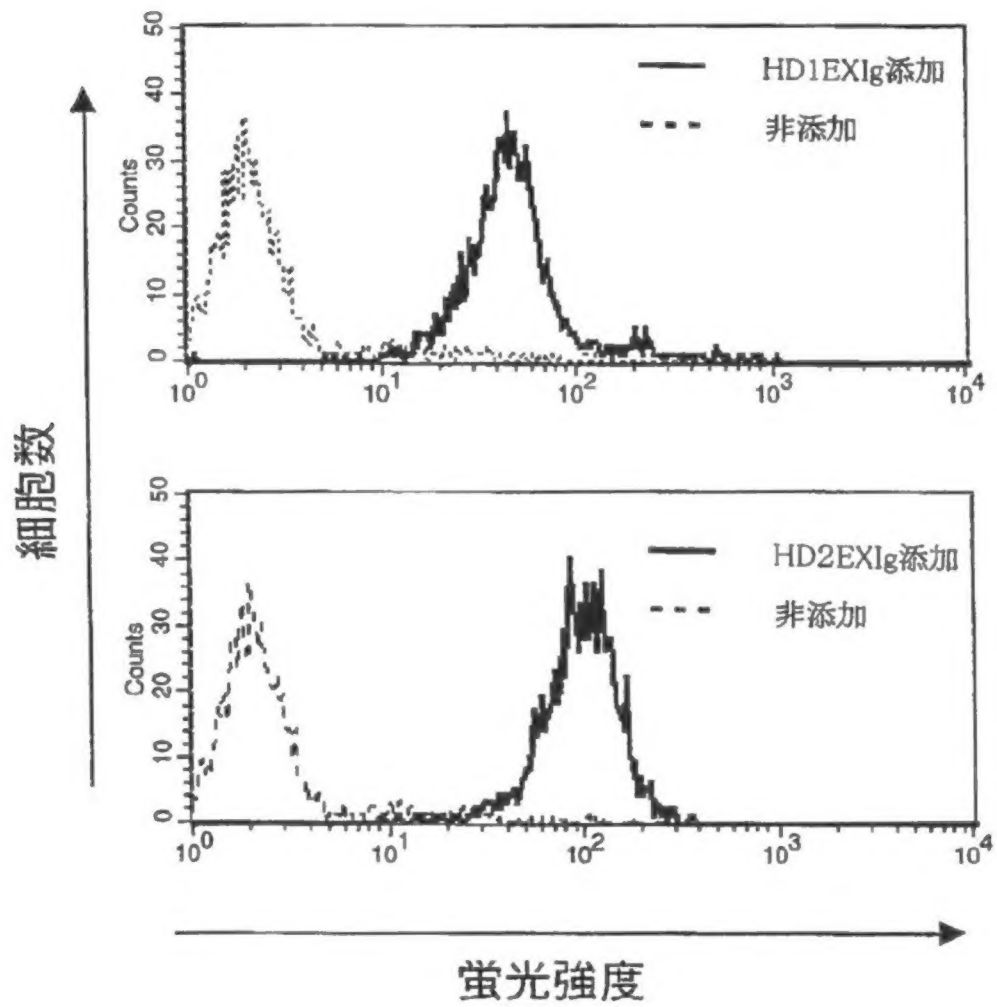
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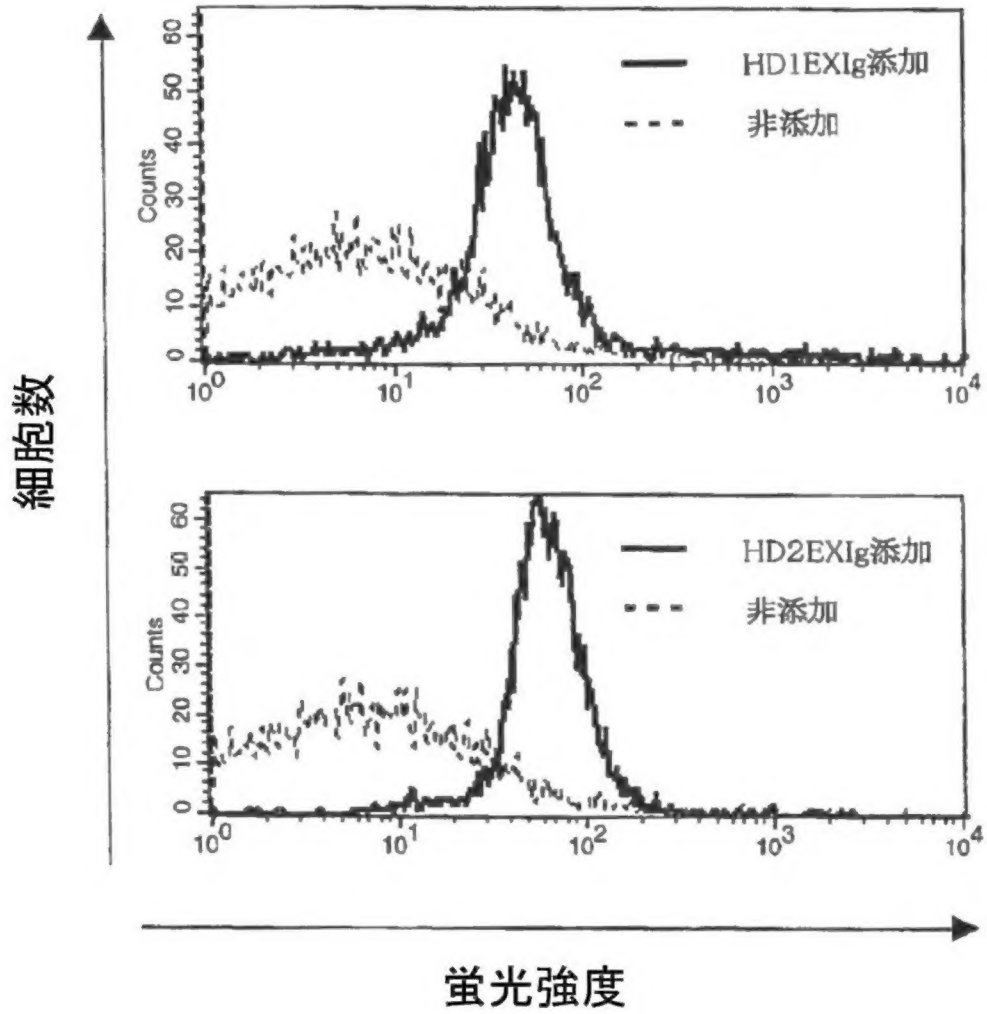


1.心臓、2.脳、3.胎盤、4.肺、5.肝臓、6.骨格筋、7.腎臓、8.脾臓
 9.脾臓、10.胸腺、11.前立腺、12.精巣、13.卵巣、14.小腸、15.結腸、16.末梢血リンパ球
 17.胃、18.甲状腺、19.脊髄、20.リンパ節、21.気管、22.副腎、23.骨髄
 24.胎児脳、25.胎児肺、26.胎児肝臓、27.胎児腎臓

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